

FHF-1	-----MAAAIASSLIRQKRQARESNS-DRVSASKRRSSPSKDG-R	38
FGF-10	-----	
FHF-4	-----MAAAIASGLIRQKRQAREQHW-DRPSASRRRSSPSKN--R	37
FHF-2	-----MAAAIASSLIRQKRQARER---EKSNAACKCVSSPSKG--K	35
FHF-3	-----MAALASSLIRQKREVREPGG-SRPVSAQRRVCP-RGT-K	36
FGF4_HUMAN	-----MS-GPGTAAVALLPAVLLALL-APWAGRGGAAAPTAPN-G	37
FGF6_HUMAN	MALGQKLFITMSRGAGRLQGTWLWLVFLGIL-VGMVVP--SPAGTRAN-N	46
FGF2_HUMAN	-----	
FGF1_HUMAN	-----	
KGF-2	-----MWKWILTHCASAFPHLPGCC-CCFLLLFLVSSVPVTC-Q	38
FGF7_HUMAN	-----MHKWILTWILPTLLYR-S-----CFHIICLVGTISLAC-N	33
ZGI_RUZFGF	-----MY-SAPSACTCLCLHFLLLCF-QVQ-----VLVAEE-N	30
FGF8_HUMAN	-----MG-SPRSALSCLLLHLLVLCL-QAQEGPGRGPALGREL-A	37
FGF5_HUMAN	-----MSLSFLLLLFFSHLILSAWAHGEKRLAPKGQPGPAATRDN	40
FGF9_HUMAN	-----MAPLGEVGNVFGVQDAVPFGNVPVLP--VDSPVLLS-D	35
FGF3_HUMAN	-----MGLIWLLLLSLLEP-----G-----WPAAGPGA	23
FHF-1	SLCERHV---LGVFSKVRFCSGR-----KRPVRRRPEPQLKGIVT	75
FGF-10	-----MASKEPQLKGIVT	13
FHF-4	GLCNGNL---VDIFSKVRIEGLK-----KRRLRRQ-DPQLKGIVT	73
FHF-2	TSCDKNK---LNVFSRVKLFSGK-----KRRRRRP-EPQLKGIVT	71
FHF-3	SLCQKQL---LILLSKVRLCGGRP-----ARPDGRP-EPQLKGIVT	73
FGF4_HUMAN	TLEAELERR-WESLVALSLARLPVAAQPK-PAVQSGAGDYLLG-IKRLR	84
FGF6_HUMAN	TLLDS--RG-WGTLLSRSRAGL---AG--E-IAGVNWESGYLVG-IKRQR	86
FGF2_HUMAN	-----MAAGSITTLPALPE-----DGGSGAFPPGHFKDPK	30
FGF1_HUMAN	-----MAEGEITTTALTE-----KFN---LPPGNYKKPK	27
KGF-2	ALGQDMVSP-EATNSSSSSFSSPSAG-----RHVRSYNHLOG-DVRWR	80
FGF7_HUMAN	DMTPEQM---ATNVNCS---SPE-----RHTRSYDMEGGDIRVR	67
ZGI_RUZFGF	VDFRID-----VEK-----QTRARDDVSRKQLRLY	55
FGF8_HUMAN	SLFRAGR---EPOGVSQOHVRE-----QSLVTDQLSRRLIRTY	72
FGF5_HUMAN	PIGSSSRQSSSSAMSSSSASSSPAASLGSGSGLEQSSSQWSPS-GRRTG	89
FGF9_HUMAN	HLGQS-----E--AGGLPRGP-----AVTDLDHLKG-ILRRR	64
FGF3_HUMAN	RLRRD-----AGG-----RGGVYEHLGG-APRRR	46
FHF-1	RLFSQQ--GYFLQMHPDGTIDGTDKENDSYTLFNLIPVGLR-VVAIQGVK	122
FGF-10	RLFSQQ--GYFLQMHPDGTIDGTDKENDSYTLFNLIPVGLR-VVAIQGVK	60
FHF-4	RLYCRQ--GYFLQMHPDGTIDGTDKDDSTNSTLFNLIPVGLR-VVAIQGVK	120
FHF-2	KLYSRQ--GYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLR-VVAIQGVQ	118
FHF-3	KLFCRQ--GFYLOANPDGSIQGTPEDTSSFTFNLIPVGLR-VVTIQSAK	120
FGF4_HUMAN	RLYCNVGIGFHLQALPDGRIGGAHADT-RDSLLELSPVERG-VVSIFGVA	132
FGF6_HUMAN	RLYCNVGIGFHLQVLPDGRISGTHEEN-PYSLLEISTVERG-VVSLFGVR	134
FGF2_HUMAN	RLYCKNG-GFFLRIPHDPGRVDGVREKSDPHIKLQLQAEERG-VVSIKGVK	78
FGF1_HUMAN	LLYCSNG-GHFLRILPDGTVDGTRDRSDQHIQLQLSAESVG-EVYIKSTE	75
KGF-2	KLFSFT--KYFLKIEKNGKVSQTKKENCPSILEITSVEIG-VVAVKAIN	127
FGF7_HUMAN	RLFCRT--QWYLRIDKRGKVKGTOEMKNNYNIMEIRTVAVG-IVAIGVE	114
ZGI_RUZFGF	QLYSRTS-GKHIQVLG-RRISARGEDGDKYAQLLVETDTFGSQVRIKKE	103
FGF8_HUMAN	QLYSRTS-GKHVQVLANKRINAMAEDGDPFAKLIVETDTFGSRVRVRGAE	121
FGF5_HUMAN	SLYCRVGIGFHLQIYPDGKVNGSHEAN-MLSVLEIFAVSQG-IVGIRGVF	137
FGF9_HUMAN	QLYCRT--GFHLEIFPNGTIQGTTRKDHRSRFGILEFISIAVG-LVSIRGVD	111
FGF3_HUMAN	KLYCAT--KYHLQLHPSGRVNGSLENS-AYSILEITAVEVG-IVAIRGLF	92
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Fig. 1

FHF-1	ASLYVAMNGEGYLYSSDV-FTPECKFKESVFENYYVIYSSTLYRQQESG-	170
FGF-10	ASLYVAMNGEGYLYSSDV-FTPECKFKESVFENYYVIYSSTLYRQQESG-	108
FHF-4	TGLYIAMNGEGYLYPSEL-FTPECKFKESVFENYYVIYSSTLYRQQESG-	168
FHF-2	TKLYLAMNSEGGLYTSEL-FTPECKFKESVFENYYVTYSSMIYRQQQSG-	166
FHF-3	LGHYAMNAEGLLYSSPH-FTAECRFKECVFENYYVLYASALYRQRRSG-	168
FGF4_HUMAN	SRFFVAMSSKGKLYGSPF-FTDECTFKEILLPNNYNAYESYKYPG-----	176
FGF6_HUMAN	SALFVAMNSKGRLYATPS-FQEECKFRETLPLNNYNAYESDLYQG-----	178
FGF2_HUMAN	ANRYLAMKEDGRLLASKC-VTDECFERLESNNYNTYRSRKYTS-----	122
FGF1_HUMAN	TGQYLAMDTDGLLYGSQT-PNEECFLERLEENHYNTYISKKHAEK--N-	121
KGF-2	SNYYLAMNKKGKLYGSKE-FNNDCKLKERIEENGYNTYASFNWQHN--G-	173
FGF7_HUMAN	SEFYLAMNKEGKLYAKKE-CNEDCNFKELILENHYNTYASAKWTHN--G-	160
ZGI_HUZFGE	TEFYLCMNRKGKLVGKPDGTSKECVFIEKVLNNYTALMSAKYSG-----	148
FGF8_HUMAN	TGLYICMNNKGKLIKASNGKGKDCVFTEIVLNNYTALQNAKYEG-----	166
FGF5_HUMAN	SNKFLAMSKKGKLIHASAK-FTDDCKFRERFQENSYNTYASAIHRTEKTG-	185
FGF9_HUMAN	SGLYLGMNEKGELYGSEK-LTQECVFREQFEENWYNTYSSNLYKHVDTG-	159
FGF3_HUMAN	SGRYLAMNKRGRLYASEH-YSAECEFVERIHELGYNTYASRLYRTVSSTP	141

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FHF-1	-----RAWFLGLNKEGQIMKG--NRVKKTKPSSHFPKPIEVCMYR	209
FGF-10	-----RAWFLGLNKEGQIMKG--NRVEKTKPSSHFPKPIEVCMYR	147
FHF-4	-----RAWFLGLNKEGQAMKG--NRVKKTKPAAHFLPKPLEVAMYR	207
FHF-2	-----RGWYLGLNKEGEIMKG--NHVKKNKPAAHFLPKPLKVAMYK	205
FHF-3	-----RAWYLGLDKEGQVMKG--NRVKKTKAAAHFLPKLLEVAMYQ	207
FGF4_HUMAN	-----MFIALSKNGKTKKG--NRVSPTMKVTHFLPRL-----	206
FGF6_HUMAN	-----TYIALSKYGRVKRG--SKVSPIMTVTHFLPRI-----	208
FGF2_HUMAN	-----WYVALKRTGQYKLG--SKTGPGQKAILFLPMSAKS----	155
FGF1_HUMAN	-----WFVGLKKNKGCKRG--PRTHYGQKAILFLPLPVSSD---	155
KGF-2	-----ROMYVALNGKGAPRRG--QKTRRKNTSAHFLPMVVHS----	208
FGF7_HUMAN	-----GEMFVALNQKGIPVRG--KKTKEQKTAHFLPMAIT----	194
ZGI_HUZFGE	-----WYVGFTKKGRPRKG--PKTRENQQDVHFMKRYPKGQPEL	185
FGF8_HUMAN	-----WYMAFTRKGRPRKG--SKTROHQREVHFMKRLPRGHHTT	203
FGF5_HUMAN	-----REWYVALNKRKGAKRGCSPRVKPOHISTHFLPRFKQSEQ-P	225
FGF9_HUMAN	-----RRYYVALNKDGTREG--TRTKRHOKFTHFLPRPVDPAKVP	198
FGF3_HUMAN	GARRQPSAERLWYVSVNGKGRPRRG--FKTRRTQKSSLFLPRVLDHRDHE	189

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FHF-1	EPSLHEIGEKGQ----GRS--RKSSGTPTMNGGKVVNQDST-----	243
FGF-10	EPSLHEIGENK----GVQ--GKFWTPP-----	168
FHF-4	EPSLHDVGETVPKP-GVTPSKSTSASAIMNGGKPVNKSCTT-----	247
FHF-2	EPSLHDLTEFSRSG-SGTPTKRSVSGVLNGGKSMHNEST-----	245
FHF-3	EPSLHSVPEAS-----P--SSPPAP-----	225
FGF4_HUMAN	-----	
FGF6_HUMAN	-----	
FGF2_HUMAN	-----	
FGF1_HUMAN	-----	
KGF-2	-----	
FGF7_HUMAN	-----	
ZGI_HUZFGE	QKPFKYTTVTK----RSRR--IRPHTPA-----	207
FGF8_HUMAN	EQSLRFEFLNYPF--TRSLRGSQRTWAPEPR-----	233
FGF5_HUMAN	ELSFTVTVPKKNP-PSPIKSKIPLSAPRKNTNSVKYRLKFRFG-----	268
FGF9_HUMAN	ELYKDILSQS-----	208
FGF3_HUMAN	MVRQLQSGLP RPPGKGVQPRRRRQKQSPDNLEPSHVQASRLGSQLEASAH	239

Fig. 2

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	1.00	0.39	0.43	0.29	0.46	0.33	0.36	0.38	0.37	0.41	0.39	0.40	0.42	0.40	0.35	0.38
2		1.00	0.38	0.34	0.41	0.35	0.38	0.33	0.38	0.44	0.39	0.37	0.37	0.39	0.35	0.60
3			1.00	0.31	0.42	0.34	0.33	0.36	0.34	0.38	0.35	0.37	0.41	0.46	0.35	0.35
4				1.00	0.34	0.53	0.26	0.24	0.26	0.31	0.28	0.30	0.30	0.31	0.28	0.32
5					1.00	0.35	0.39	0.43	0.39	0.39	0.43	0.42	0.44	0.43	0.40	0.43
6						1.00	0.33	0.31	0.33	0.31	0.32	0.34	0.34	0.32	0.36	0.36
7							1.00	0.34	0.98	0.33	0.76	0.81	0.34	0.37	0.67	0.42
8								1.00	0.34	0.54	0.34	0.37	0.36	0.36	0.34	0.38
9									1.00	0.33	0.66	0.72	0.34	0.37	0.62	0.42
10										1.00	0.32	0.35	0.40	0.37	0.32	0.43
11											1.00	0.68	0.36	0.38	0.58	0.41
12												1.00	0.36	0.33	0.62	0.42
13													1.00	0.47	0.34	0.32
14														1.00	0.30	0.31
15															1.00	0.38
16																1.00

Fig. 3